

SHF

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,330A

DATE: 06/22/2001

TIME: 12:11:11

Input Set : A:\ES.txt

Output Set: N:\CRF3\06222001\I674330A.raw

3 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.
 5 <120> TITLE OF INVENTION: A NOVEL POLYPEPTIDE, A CDNA ENCODING THE POLYPEPTIDE AND
 UTILIZATION

6 THEREOF
 8 <130> FILE REFERENCE: Q61536
 10 <140> CURRENT APPLICATION NUMBER: 09/674,330A
 11 <141> CURRENT FILING DATE: 2000-10-30
 13 <150> PRIOR APPLICATION NUMBER: JP 10-119731
 14 <151> PRIOR FILING DATE: 1998-04-28
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02283
 17 <151> PRIOR FILING DATE: 1999-04-28
 19 <160> NUMBER OF SEQ ID NOS: 12
 21 <170> SOFTWARE: PatentIn version 3.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1344
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mus musculus
 28 <400> SEQUENCE: 1

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31 gggautgcac ageagcagtg cacaacggc tttgacctgg acggccagtc aggacagtgt	120
33 cttagatattg atgaatcccg gaccateccct gaggtttgtc gtggggacat gatgtgtgtc	180
35 aaccagaatg ggggttattt gtgcateccct cgaaccaaacc cagtgtatcg agggccttac	240
37 taaaatccct actctacate ctactcaggc ccataccccag cagggcccccc accagtacca	300
39 gtttccaaact accccacgat ttcaaggect cttgtctgcc gctttgggtt tcagatggat	360
41 qaaggcaacc aqgtgtgqa tggacggag tggcaacag actcacacca gtgcacccct	420
43 acccagatct gtatcaacac tgaaggaggt tacacctgtt cctgcacccg tgggtactgg	480
45 ctgttggaaq ggcagtgcct agatatttgat gaatgtgtt atggttactgg ccagcagctc	540
47 tttgtccaaatg ttccaggatc ctatccctgt acatgcaacc ctggtttccat cttcaacgac	600
49 gatgtqaagggt ttggccaaaga tggaaacggag tggaaactgt agaateccctg tggcaagacc	660
51 tttgtcaaca cttatgctc ttcatctgc cgctgtgacc caggatatga acttgaggaa	720
53 gatqqccatcc actqcagtga tatggacggag tgcagttctt cccgatcttct ctgtcaacac	780
55 qagtgtgtqa accagccggg ctcatacttc tgcctgtgcc ctccaggatc cgtccctgtq	840
57 gatgataacc gaaqctqcca ggtatcaat gaatgtgagc accqaaacca caccgtgtacc	900
59 tcactgcaga cttgttacaa ttacaaggqg qqcttcaaat gtattgtatc catcagetgt	960
61 qaggqagcctt atctgtgtat tggtaaaac cgctgtatgt gtcctgtqa gcacaccage	1020
63 ttcacqagaccc agccatccac cttatgtat cgggacatgg atgtgggtgtc aqgacgatcc	1080
65 ttgttctgtq acatcttccaa gatgcaagca acaacccgat accctgtgtc ctattacatt	1140
67 ttccagatca aatctgqcaa cggggatcga gagttctata tgcggcaaac agggcttac	1200
69 autqccaccc tggatgtgac acggccatcc aaaggccctc qggacatcca qctqgacttg	1260
71 qagatgtatca ctgtcaacac tgcatacaac ttcaaggagca qtcctgtatcc cccactgegg	1320
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76 <210> SEQ ID NO: 2

77 <211> LENGTH: 2233

78 <212> TYPE DNA

79 <213> ORGANISM: Mus musculus

81 <220> FEATURE:

82 <221> NAME/KEY misc_feature

83 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart

ENTERED

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86 <220> FEATURE:
 87 <221> NAME/KEY: misc_feature
 88 <222> OTHER INFORMATION: "n" may be either a, c, g or t
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 92 <221> NAME/KEY: CDS
 93 <222> LOCATION: (75)..(1418)
 95 <220> FEATURE:
 96 <221> NAME/KEY: sig_peptide
 97 <222> LOCATION: (75)..(143)
 99 <220> FEATURE:
 100 <221> NAME/KEY: mat_peptide
 101 <222> LOCATION: (144)..()
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 106 cggcgatctt ggtat atg cca gga tta aaa agg ata ctc act gtt acc atc 110
 107 Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
 108 -20 -15
 110 ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca 158
 111 Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
 112 -10 -5 -1 1 5
 114 aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
 115 Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
 116 10 15 20
 118 qaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atq tgt gtc 254
 119 Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
 120 25 30 35
 122 aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
 123 Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
 124 40 45 50
 126 cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350
 127 Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
 128 55 60 65
 130 cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398
 131 Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
 132 70 75 80 85
 134 agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag 446
 135 Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln
 136 90 95 100
 138 tgt gtg gat gtg gac gag tgt gca aca gac tca cac caq tgc aac cct 494
 139 Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro
 140 105 110 115
 142 acc caq atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc 542
 143 Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr
 144 120 125 130
 146 gat ggg tac tgg ctt ctg gaa ggg caq tuc cta gat att gat gaa tgt 590
 147 Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys
 148 135 140 145
 150 cgc tat ggt tac tgc caq caq ctc tgt gca aat gtt cca gga tcc tat 638
 151 Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr

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152	150	155	160	165													
154	tcc	tgt	aca	tgc	aac	cct	ggc	ttc	acc	ctc	aac	gac	qat	gga	aqg	tct	686
155	Ser	Cys	Thr	Cys	Asn	Pro	Gly	Phe	Thr	Leu	Asn	Asp	Asp	Gly	Arg	Ser	
156								170		175						180	
158	tgc	caa	gat	gtg	aac	gag	tgc	gaa	act	gag	aat	ccc	tgt	gtt	cag	acc	734
159	Cys	Gln	Asp	Val	Asn	Glu	Cys	Glu	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	
160								185		190						195	
162	tgt	gtc	aac	acc	tat	ggc	tct	ttc	atc	tgc	cgc	tgt	gac	cca	gga	tat	782
163	Cys	Val	Asn	Ihr	Tyr	Gly	Ser	Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	
164								200		205						210	
166	gaa	ctt	gag	gaa	gat	ggc	att	cac	tgc	agt	gat	atg	gac	gag	tgc	agc	830
167	Glu	Leu	Glu	Glu	Asp	Gly	Ile	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	
168								215		220						225	
170	ttc	tcc	gag	tgc	ctc	tgt	caa	cac	gag	tgt	gtg	aac	cag	cgc	ggc	tca	878
171	Phe	Ser	Glu	Phe	Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Ser	
172								230		235						240	245
174	tac	ttc	tgc	tgc	cct	cca	ggc	tac	gtc	ctg	ttg	gat	gat	aac	cga	926	
175	Tyr	Phe	Cys	Ser	Cys	Pro	Pro	Gly	Tyr	Val	Leu	Leu	Asp	Asp	Asn	Arg	
176								250		255						260	
178	agc	tgc	cag	gat	atc	aat	gaa	tgt	gag	cac	cga	aac	cac	acg	tgt	acc	974
179	Ser	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Glu	His	Arg	Asn	His	Thr	Cys	Thr	
180								265		270						275	
182	tca	ctg	cag	act	tgc	tac	aat	cta	caa	qqq	ggc	ttc	aaa	tgt	att	gat	1022
183	Ser	Leu	Gln	Thr	Cys	Tyr	Asn	Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	
184								280		285						290	
186	ccc	atc	agc	tgt	gag	gag	cct	tat	ctg	ctg	att	gtt	gaa	aac	cgc	tgt	1070
187	Pro	Ile	Ser	Cys	Gln	Glu	Pro	Tyr	Leu	Leu	Ile	Gly	Glu	Asn	Arg	Cys	
188								295		300						305	
190	atg	tgt	cct	gct	gag	cac	acc	agc	tgc	aga	gac	cag	cca	ttc	acc	atc	1118
191	Met	Cys	Pro	Ala	Gln	His	Thr	Ser	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	
192								310		315						320	325
194	ctg	tat	cgj	gac	atg	qat	gtg	gtg	tca	gga	cgc	tcc	gtt	cct	gtc	gac	1166
195	Leu	Tyr	Arg	Asp	Met	Asp	Val	Val	Ser	Gly	Arg	Ser	Vai	Pro	Ala	Asp	
196								330		335						340	
198	atc	ttc	cag	atg	caa	qca	aca	acc	cga	tac	cct	ggc	tat	tac	att	1214	
199	Ile	Phe	Gln	Met	Gln	Ala	Ihr	Thr	Arg	Tyr	Pro	Gly	Ala	Tyr	Ile		
200								345		350						355	
202	ttc	cag	atc	aaa	tct	ggc	aac	qag	qgt	cqa	gag	ttc	tat	atg	cgg	caa	1262
203	Phe	Gln	Ile	Lys	Ser	Gly	Asn	Glu	Gly	Arg	Glu	Phe	Tyr	Met	Arg	Gln	
204								360		365						370	
206	aca	ggg	cct	atc	agt	gcc	acc	ctg	gtg	atg	aca	cgc	ccc	atc	aaa	ggg	1310
207	Thr	Gly	Pro	Ile	Ser	Ala	Thr	Leu	Val	Met	Thr	Arg	Pro	Ile	Lys	Gly	
208								375		380						385	
210	cct	cgg	gac	atc	caq	ctg	qac	ttq	gag	atq	atc	act	gtc	aac	act	gtc	1358
211	Pro	Arg	Asp	Ile	Gln	Leu	Asp	Leu	Glu	Met	Ile	Thr	Val	Asn	Thr	Val	
212								390		395						400	405
214	atc	aac	ttc	aga	qgc	aqc	tcc	qtq	atc	cqa	ctg	cgg	ata	tat	qtq	tcg	1406
215	Ile	Asn	Phe	Arg	Gly	Ser	Ser	Val	Ile	Arg	Leu	Arg	Ile	Tyr	Val	Ser	
216								410		415						420	

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218 cag tat ccg ttc tqaqccttg yctaaggct ctqacactgc cttcaccag	1458
219 Gln Tyr Pro Phe	
220 425	
221 caccgaggga cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac	1518
224 ctttctgtgt gtaatactcc tggggcata aqcttagcat cttgaccat atctgtacta	1578
226 ttgcagatgg tcactctgaa qgacacccctg ccctcagttc ctatgtqca gttatccaaa	1638
228 agtgttcattc tttagccccctg atatgagtt gcccagtqact cttcaaaqcc ttcattttat	1698
230 ttcattcgtt ttataaaaaaa gaaaaataaat tagatttgc ggggtatyaq ttcctcgaagg	1758
232 ttcaaaagac tgagtggctt getctcacct cttctctcc ttcctccate ttttgcqca	1818
234 ttgcgtgtttt gcaaaaagtc tcatgggctc gtggaaatq ctggaaatag ctatgttqct	1878
236 tcttgcattgt tcttgcataagg ctatgggaaac acaccacage aggatcgaq gtttttatag	1938
238 agtctattttt aaaatccat ctggtattttt cagcataaaaa gaaatttttag ttgtctttaa	1998
240 aatttgcattg agtgcgttaac cttttttttt tcatgttgc gtttcttaaa gtggtagaat	2058
242 ttcattccaaa ggcctcagat acatgttgc ttcagtcattt ccaacctccat ctttgc	2118
W--> 244 atcttagccc agttttacg aagaccctt aatcatgctt nttaagagt ttttacccaa	2178
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249 <210> SEQ ID NO: 3	
250 <211> LENGTH: 448	
251 <212> TYPE: PRT	
252 <213> ORGANISM: Mus musculus	
254 <220> FEATURE:	
255 <221> NAME/KEY: misc_feature	
256 <223> OTHER INFORMATION: Clone mouse A55 derived from Day 13 mouse embryonic heart	
258 <400> SEQUENCE: 3	
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264 Leu Pro His Pro Gly Asn Ala Gln Gln Cys Thr Asn Gly Phe Asp	
265 -5 -1 1 5	
268 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr	
269 10 15 20 25	
272 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly	
273 30 35 40	
276 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr	
277 45 50 55	
280 Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala	
281 60 65 70	
284 Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val	
285 75 80 85	
288 Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val	
289 90 95 100 105	
292 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys	
293 110 115 120	
296 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp	
297 125 130 135	
300 Leu Leu Glu Gly Gin Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr	
301 140 145 150	
304 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys	
305 155 160 165	
308 Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val	

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309	170	175	180	185												
312	Asn	Glu	Cys	Glu	Ihr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr
313					190				195						200	
316	Tyr	Gly	Ser	Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu
317						205				210					215	
320	Asp	Gly	Ile	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu	Phe
321						220			225					230		
324	Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Ser	Tyr	Phe	Cys	Ser
325						235			240					245		
328	Cys	Pro	Pro	Gly	Tyr	Val	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp
329		250				255				260					265	
332	Ile	Asn	Glu	Cys	Glu	His	Arg	Asn	His	Ihr	Cys	Thr	Ser	Leu	Gln	Thr
333						270				275					280	
336	Cys	Tyr	Asn	Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Ser	Cys
337						285			290					295		
340	Glu	Glu	Pro	Tyr	Leu	Leu	Ile	Gly	Glu	Asn	Arg	Cys	Met	Cys	Pro	Ala
341						300			305					310		
344	Glu	His	Thr	Ser	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp
345						315			320					325		
348	Met	Asp	Val	Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	Ile	Phe	Gln	Met
349						330			335			340			345	
352	Gln	Ala	Thr	Thr	Arg	Tyr	Pro	Gly	Ala	Tyr	Tyr	Ile	Phe	Gln	Ile	Lys
353						350				355					360	
356	Ser	Gly	Asn	Glu	Gly	Arg	Glu	Phe	Tyr	Met	Arg	Gln	Thr	Gly	Pro	Ile
357						365				370					375	
360	Ser	Ala	Thr	Leu	Val	Met	Thr	Arg	Pro	Ile	Lys	Gly	Pro	Arg	Asp	Ile
361						380			385			390				
364	Gln	Leu	Asp	Leu	Glu	Met	Ile	Thr	Val	Asn	Thr	Val	Ile	Asn	Phe	Arg
365						395			400			405				
368	Gly	Ser	Ser	Val	Ile	Arg	Leu	Arg	Ile	Tyr	Val	Ser	Gln	Tyr	Pro	Phe
369						410			415			420			425	
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373	->211-	LENGTH:	423													
374	->212-	TYPE:	PRT													
375	->213-	ORGANISM:	Mus musculus													
377	->400-	SEQUENCE:	4													
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380	1				5				10						15	
382	Asp	Ile	Asp	Glu	Cys	Arg	Thr	Ile	Pro	Glu	Ala	Cys	Arg	Cly	Asp	Met
383					20				25						30	
385	Met	Cys	Val	Asn	Gln	Asn	Gly	Gly	Tyr	Leu	Cys	Ile	Pro	Arg	Thr	Asn
386					35				40					45		
388	Fro	Val	Tyr	Arg	Gly	Pro	Tyr	Ser	Asn	Pro	Tyr	Ser	Ihr	Ser	Tyr	Ser
389					50			55			60					
391	Gly	Pro	Tyr	Pro	Ala	Ala	Pro	Pro	Val	Pro	Ala	Ser	Asn	Tyr	Pro	
392	65				70				75					80		
394	Thr	Ile	Ser	Arg	Pro	Leu	Val	Cys	Arg	Phe	Gly	Tyr	Gln	Met	Asp	Glu
395					85				90					95		
397	GLY	Asn	Gln	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Asp	Ser	His	Gln

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:1029 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11

L:1029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11